

1 / 3 4

SEQUENCE LISTING

<110> Oncotherapy Science, Inc.

The University of Tokyo

<120> Method of Diagnosing Breast Cancer

<130> ONC-A0306P1

<160> 34

<170> PatentIn version 3.1

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<213> Homo sapiens

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gggatc atg cag aga gct tca cgt ctg aag aga gag ctg cac atg tta 168

2 / 3 4

Met Gln Arg Ala Ser Arg Leu Lys Arg Glu Leu His Met Leu
1 5 10

gcc aca gag cca ccc cca ggc atc aca tgt tgg caa gat aaa gac caa 216
Ala Thr Glu Pro Pro Pro Gly Ile Thr Cys Trp Gln Asp Lys Asp Gln
15 20 25 30

atg gat gac ctg cga gct caa ata tta ggt gga gcc aac aca cct tat 264
Met Asp Asp Leu Arg Ala Gln Ile Leu Gly Gly Ala Asn Thr Pro Tyr
35 40 45

gag aaa ggt gtt ttt aag cta gaa gtt atc att cct gag agg tac cca 312
Glu Lys Gly Val Phe Lys Leu Glu Val Ile Ile Pro Glu Arg Tyr Pro
50 55 60

ttt gaa cct cct cag atc cga ttt ctc act cca att tat cat cca aac 360
Phe Glu Pro Pro Gln Ile Arg Phe Leu Thr Pro Ile Tyr His Pro Asn
65 70 75

att gat tct gct gga agg att tgt ctg gat gtt ctc aaa ttg cca cca 408
Ile Asp Ser Ala Gly Arg Ile Cys Leu Asp Val Leu Lys Leu Pro Pro
80 85 90

aaa ggt gct tgg aga cca tcc ctc aac atc gca act gtg ttg acc tct 456
Lys Gly Ala Trp Arg Pro Ser Leu Asn Ile Ala Thr Val Leu Thr Ser
95 100 105 110

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130 135 140

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Ala Arg Gln Trp Thr Glu Lys His Ala Arg Gln Lys Gln Lys Ala Asp
145 150 155

gag gaa gag atg ctt gat aat cta cca gag gct ggt gac tcc aga gta 648
Glu Glu Glu Met Leu Asp Asn Leu Pro Glu Ala Gly Asp Ser Arg Val
160 165 170

cac aac tca aca cag aaa agg aag gcc agt cag cta gta ggc ata gaa 696
His Asn Ser Thr Gln Lys Arg Lys Ala Ser Gln Leu Val Gly Ile Glu
175 180 185 190

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Lys Lys Phe His Pro Asp Val
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tgttcttgc caaggtgatc taagttgcct accttgaatt ttttttaaa tatatttgat 810

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Asp Leu Arg Ala Gln Ile Leu Gly Gly Ala Asn Thr Pro Tyr Glu Lys

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Gly Val Phe Lys Leu Glu Val Ile Ile Pro Glu Arg Tyr Pro Phe Glu

5 / 3 4

50

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60

Pro Pro Gln Ile Arg Phe Leu Thr Pro Ile Tyr His Pro Asn Ile Asp

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Ser Ala Gly Arg Ile Cys Leu Asp Val Leu Lys Leu Pro Pro Lys Gly

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Ala Trp Arg Pro Ser Leu Asn Ile Ala Thr Val Leu Thr Ser Ile Gln

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Leu Leu Met Ser Glu Pro Asn Pro Asp Asp Pro Leu Met Ala Asp Ile

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Ser Ser Glu Phe Lys Tyr Asn Lys Pro Ala Phe Leu Lys Asn Ala Arg

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Gln Trp Thr Glu Lys His Ala Arg Gln Lys Gln Lys Ala Asp Glu Glu

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150

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160

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Glu Met Leu Asp Asn Leu Pro Glu Ala Gly Asp Ser Arg Val His Asn

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Phe His Pro Asp Val

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ggc tct cgg cgc cgg cgc cag cgc ccc tct gtg ggc gtc cag tcc ttg 154

Gly Ser Arg Arg Arg Arg Gln Arg Pro Ser Val Gly Val Gln Ser Leu

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agg ccg cag agc ccg cag ctc agg cag agc gac ccg cag aaa cgg aac 202

Arg Pro Gln Ser Pro Gln Leu Arg Gln Ser Asp Pro Gln Lys Arg Asn

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ctg gac ctg gag aaa agc ctg cag ttc ctg cag cag cac tcg gag 250

Leu Asp Leu Glu Lys Ser Leu Gln Phe Leu Gln Gln Gln His Ser Glu

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atg ctg gcc aag ctc cat gag gag atc gag cat ctg aag cgg gaa aac 298

Met Leu Ala Lys Leu His Glu Glu Ile Glu His Leu Lys Arg Glu Asn

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aag gat ctc cat tac aag ctc ata atg aat cag aca tca cag aag aaa 346

Lys Asp Leu His Tyr Lys Leu Ile Met Asn Gln Thr Ser Gln Lys Lys

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90

95

8 / 3 4

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Asp Gly Pro Ser Gly Asn His Leu Ser Arg Ala Ser Ala Pro Leu Gly

100 105 110

gct cgc tgg gtc tgc atc aac gga gtg tgg gta gag ccg gga gga ccc 442
Ala Arg Trp Val Cys Ile Asn Gly Val Trp Val Glu Pro Gly Gly Pro
115 120 125 130

agc cct gcc agg ctg aag gag ggc tcc tca cgg aca cac agg cca gga 490
Ser Pro Ala Arg Leu Lys Glu Gly Ser Ser Arg Thr His Arg Pro Gly
135 140 145

ggc aag cgt ggg cgt ctt gcg ggc ggt agc gcc gac act gtg cgc tct 538
Gly Lys Arg Gly Arg Leu Ala Gly Gly Ser Ala Asp Thr Val Arg Ser
150 155 160

cct gca gac agc ctc tcc atg tca agc ttc cag tct gtc aag tcc atc 586
Pro Ala Asp Ser Leu Ser Met Ser Ser Phe Gln Ser Val Lys Ser Ile
165 170 175

tct aat tca ggc aag gcc agg ccc cag ccc ggc tcc ttc aac aag caa 634
Ser Asn Ser Gly Lys Ala Arg Pro Gln Pro Gly Ser Phe Asn Lys Gln
180 185 190

gat tca aaa gct gac gtc tcc cag aag gcg gac ctg gaa gag gag ccc 682
Asp Ser Lys Ala Asp Val Ser Gln Lys Ala Asp Leu Glu Glu Pro

9 / 3 4

195	200	205	210	
ct a ct t c a c a a c a g c a a g ct g g a c a a a g t t c c t g g g g t a c a a g g g c a g				730
Leu Leu His Asn Ser Lys Leu Asp Lys Val Pro Gly Val Gln Gly Gln				
215	220	225		
g c c a g a a g g a g a a a g c a g a g g c c t c t a a t g c a g g a g c t g c c t g t a t g				778
Ala Arg Lys Glu Lys Ala Glu Ala Ser Asn Ala Gly Ala Ala Cys Met				
230	235	240		
g g g a a c a g c c a g c a c a g g g c a g a g g a t g g g g c g g g c a c a c c c				826
Gly Asn Ser Gln His Gln Gly Arg Gln Met Gly Ala Gly Ala His Pro				
245	250	255		
c c a a t g a t c c t g c c c c t t c c c c t g c g a a g c c c a c c a c t t a g g c a g				874
Pro Met Ile Leu Pro Leu Pro Leu Arg Lys Pro Thr Thr Leu Arg Gln				
260	265	270		
t g c g a a g t g c t c a t c c g c g a g c t g t g g a a t a c c a a c c t c c t g c a g a c c				922
Cys Glu Val Leu Ile Arg Glu Leu Trp Asn Thr Asn Leu Leu Gln Thr				
275	280	285	290	
c a a g a g c t g c g g c a c c t c a a g t c c c t g g a a g g g a g c c a g a g g c c c				970
Gln Glu Leu Arg His Leu Lys Ser Leu Leu Glu Gly Ser Gln Arg Pro				
295	300	305		

1 0 / 3 4

cag gca gcc ccg gag gaa gct agc ttt ccc agg gac caa gaa gcc acg 1018
Gln Ala Ala Pro Glu Glu Ala Ser Phe Pro Arg Asp Gln Glu Ala Thr

310 315 320

cat ttc ccc aag gtc tcc acc aag agc ctc tcc aag aaa tgc ctg agc 1066
His Phe Pro Lys Val Ser Thr Lys Ser Leu Ser Lys Lys Cys Leu Ser

325 330 335

cca cct gtg gcg gag cgt gcc atc ctg ccc gca ctg aag cag acc ccg 1114
Pro Pro Val Ala Glu Arg Ala Ile Leu Pro Ala Leu Lys Gln Thr Pro

340 345 350

aag aac aac ttt gcc gag agg cag aag agg ctg cag gca atg cag aaa 1162
Lys Asn Asn Phe Ala Glu Arg Gln Lys Arg Leu Gln Ala Met Gln Lys

355 360 365 370

cgg cgc ctg cat cgc tca gtg ctt tga gccaccccaa tctggcgtcagt 1209
Arg Arg Leu His Arg Ser Val Leu

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gccaggccca ccaacctgca gctggagact ggctctctat agcatttcct gatacttcg 1269

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Ser Leu Arg Pro Gln Ser Pro Gln Leu Arg Gln Ser Asp Pro Gln Lys

35

40

45

Arg Asn Leu Asp Leu Glu Lys Ser Leu Gln Phe Leu Gln Gln His

50

55

60

1 2 / 3 4

Ser Glu Met Leu Ala Lys Leu His Glu Glu Ile Glu His Leu Lys Arg

65 70 75 80

Glu Asn Lys Asp Leu His Tyr Lys Leu Ile Met Asn Gln Thr Ser Gln

85 90 95

Lys Lys Asp Gly Pro Ser Gly Asn His Leu Ser Arg Ala Ser Ala Pro

100 105 110

Leu Gly Ala Arg Trp Val Cys Ile Asn Gly Val Trp Val Glu Pro Gly

115 120 125

Gly Pro Ser Pro Ala Arg Leu Lys Glu Gly Ser Ser Arg Thr His Arg

130 135 140

Pro Gly Gly Lys Arg Gly Arg Leu Ala Gly Gly Ser Ala Asp Thr Val

145 150 155 160

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Arg Ser Pro Ala Asp Ser Leu Ser Met Ser Ser Phe Gln Ser Val Lys

165

170

175

Ser Ile Ser Asn Ser Gly Lys Ala Arg Pro Gln Pro Gly Ser Phe Asn

180

185

190

Lys Gln Asp Ser Lys Ala Asp Val Ser Gln Lys Ala Asp Leu Glu Glu

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205

Glu Pro Leu Leu His Asn Ser Lys Leu Asp Lys Val Pro Gly Val Gln

210

215

220

Gly Gln Ala Arg Lys Glu Lys Ala Glu Ala Ser Asn Ala Gly Ala Ala

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235

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Cys Met Gly Asn Ser Gln His Gln Gly Arg Gln Met Gly Ala Gly Ala

245

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His Pro Pro Met Ile Leu Pro Leu Pro Leu Arg Lys Pro Thr Thr Leu

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265

270

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Arg Gln Cys Glu Val Leu Ile Arg Glu Leu Trp Asn Thr Asn Leu Leu

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280

285

Gln Thr Gln Glu Leu Arg His Leu Lys Ser Leu Leu Glu Gly Ser Gln

290

295

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Arg Pro Gln Ala Ala Pro Glu Glu Ala Ser Phe Pro Arg Asp Gln Glu

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315

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Ala Thr His Phe Pro Lys Val Ser Thr Lys Ser Leu Ser Lys Lys Cys

325

330

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Leu Ser Pro Pro Val Ala Glu Arg Ala Ile Leu Pro Ala Leu Lys Gln

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Gln Lys Arg Arg Leu His Arg Ser Val Leu

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aagcgcgggt gaagcgcgca ggtcggagtg acagctgcgc tgccggcccg gctgcggta 240

gcaacgcgcc atg gac gca gag ctg gca gag gtg cgc gcc ttg caa gct 289

Met Asp Ala Glu Leu Ala Glu Val Arg Ala Leu Gln Ala

1 6 / 3 4

gag atc gcg gcc ctg cgg cga gcg tgt gag gac cca ccg gcg ccc tgg 337

Glu Ile Ala Ala Leu Arg Arg Ala Cys Glu Asp Pro Pro Ala Pro Trp

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gaa gag aag tcc cga gtc caa aaa tct ttt caa gcc ata cac caa ttc 385

Glu Glu Lys Ser Arg Val Gln Lys Ser Phe Gln Ala Ile His Gln Phe

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aat ttg gaa gga tgg aag tct tca aaa gat ctg aaa aat cag ctt gga 433

Asn Leu Glu Gly Trp Lys Ser Ser Lys Asp Leu Lys Asn Gln Leu Gly

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cat tta gaa tca gaa ctt tca ttt cta agt acg ctt act ggc atc aat 481

His Leu Glu Ser Glu Leu Ser Phe Leu Ser Thr Leu Thr Gly Ile Asn

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ata aga aat cac tcc aag cag aca gaa gac cta aca agc act gag atg 529

Ile Arg Asn His Ser Lys Gln Thr Glu Asp Leu Thr Ser Thr Glu Met

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aca gaa aag agt att aga aaa gtt cta cag aga cac aga tta tca gga 577

Thr Glu Lys Ser Ile Arg Lys Val Leu Gln Arg His Arg Leu Ser Gly

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aat tgc cac atg gtt aca ttt caa ctt gaa ttt cag att ctg gaa att 625

17 / 34

Asn Cys His Met Val Thr Phe Gln Leu Glu Phe Gln Ile Leu Glu Ile

110 115 120 125

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Gln Asn Lys Glu Arg Leu Ser Ser Ala Val Thr Asp Leu Asn Ile Ile

130 135 140

atg gag ccc aca gaa tgc tca gaa tta agt gaa ttt gtg tct aga gca 721

Met Glu Pro Thr Glu Cys Ser Glu Leu Ser Glu Phe Val Ser Arg Ala

145 150 155

gaa gag aga aaa gat ctg ttc atg ttt ttc cga agc ctg cat ttt ttt 769

Glu Glu Arg Lys Asp Leu Phe Met Phe Phe Arg Ser Leu His Phe Phe

160 165 170

gtg gag tgg ttt gaa tat cgt aag cgc acg ttt aaa cat ctc aag gaa 817

Val Glu Trp Phe Glu Tyr Arg Lys Arg Thr Phe Lys His Leu Lys Glu

175 180 185

aag tac cca gat gcc gtg tac ctc tcg gag ggg ccc tcc tcc tgc tcc 865

Lys Tyr Pro Asp Ala Val Tyr Leu Ser Glu Gly Pro Ser Ser Cys Ser

190 195 200 205

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Met Gly Ile Arg Ser Ala Ser Arg Pro Gly Phe Glu Leu Val Ile Val

210 215 220

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Trp Arg Ile Gln Ile Asp Glu Asp Gly Lys Val Phe Pro Lys Leu Asp

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230

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ctt ctc acc aaa gtc cca cag cga gcc ctg gag ctg gac aag aac aga 1009

Leu Leu Thr Lys Val Pro Gln Arg Ala Leu Glu Leu Asp Lys Asn Arg

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gcc ata gaa act gct cct ctc agc ttc cga acc ctg gta gga ctg ctt 1057

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gga atc gaa gct gct ctg gaa agc ctg ata aaa tcg ctt tgt gca gag 1105

Gly Ile Glu Ala Ala Leu Glu Ser Leu Ile Lys Ser Leu Cys Ala Glu

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gag aac aac tagttccaaa acagtgaacg tggaggatga agatgctgcg 1154

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tggaggaaca tgcaatttta ttcaatataa acatttgcta ttttctgctt agaaaccaca 1214

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<213> Homo sapiens

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35 40 45

Gly Trp Lys Ser Ser Lys Asp Leu Lys Asn Gln Leu Gly His Leu Glu

50 55 60

Ser Glu Leu Ser Phe Leu Ser Thr Leu Thr Gly Ile Asn Ile Arg Asn

20 / 34

65 70 75 80

His Ser Lys Gln Thr Glu Asp Leu Thr Ser Thr Glu Met Thr Glu Lys

85 90 95

Ser Ile Arg Lys Val Leu Gln Arg His Arg Leu Ser Gly Asn Cys His

100 105 110

Met Val Thr Phe Gln Leu Glu Phe Gln Ile Leu Glu Ile Gln Asn Lys

115 120 125

Glu Arg Leu Ser Ser Ala Val Thr Asp Leu Asn Ile Ile Met Glu Pro

130 135 140

Thr Glu Cys Ser Glu Leu Ser Glu Phe Val Ser Arg Ala Glu Glu Arg

145 150 155 160

Lys Asp Leu Phe Met Phe Phe Arg Ser Leu His Phe Phe Val Glu Trp

165 170 175

21 / 34

Phe Glu Tyr Arg Lys Arg Thr Phe Lys His Leu Lys Glu Lys Tyr Pro

180

185

190

Asp Ala Val Tyr Leu Ser Glu Gly Pro Ser Ser Cys Ser Met Gly Ile

195

200

205

Arg Ser Ala Ser Arg Pro Gly Phe Glu Leu Val Ile Val Trp Arg Ile

210

215

220

Gln Ile Asp Glu Asp Gly Lys Val Phe Pro Lys Leu Asp Leu Leu Thr

225

230

235

240

Lys Val Pro Gln Arg Ala Leu Glu Leu Asp Lys Asn Arg Ala Ile Glu

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255

Thr Ala Pro Leu Ser Phe Arg Thr Leu Val Gly Leu Leu Gly Ile Glu

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22 / 34

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23 / 34

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26 / 34

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27 / 34

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19

<210> 34

<211> 19

<212> DNA

<213> Artificial

<220>

<223> target sequence for siRNA

<400> 34

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19